

nucleotides” is found, *inter alia*, in the sequences set forth as SEQ ID NO:39, SEQ ID NO:42, and SEQ ID NO:44. The sequence of SEQ ID NO:39 is 289 nucleotides in length; the sequence of SEQ ID NO:42 is 866 nucleotides in length; and the sequence of SEQ ID NO:44 is 599 nucleotides in length. The sequences of SEQ ID NO:39, SEQ ID NO:42, and SEQ ID NO:44 were disclosed in the originally filed application as exons of Gene 214 (original Figures 10A-10B). The sequence of Gene 214 is included in SEQ ID NO:1. Accordingly, SEQ ID NO:39, SEQ ID NO:42, and SEQ ID NO:44 represent nucleotide sequences that comprise 289 or more contiguous nucleotides of SEQ ID NO:1.

For claims 34 and 56, support for the recitation of “500 or more contiguous nucleotides” is found, *inter alia*, on page 5, lines 6-9 of the originally filed specification.

For claims 37, 46, 59, and 68, support for the recitation of “vector comprising” is found, *inter alia*, on page 22, lines 19-20 of the originally filed specification.

For claims 38, 48, 60, and 70, support for the recitation of “host cell comprising” is found, *inter alia*, on page 70, lines 9-14 to page 71, lines 5-8 of the originally filed specification. This section of the application discloses that a host cell of the invention may include more than one vector/nucleic acid. Inherently, this teaches that a host cell of the invention may “comprise” a vector/nucleic acid.

For claim 52, support for the recitation of “at least 25 contiguous nucleotides” is found, *inter alia*, on page 83, lines 10-13 of the originally filed specification. A nucleic acid comprising at least 25 contiguous nucleotides of SEQ ID NO:48, SEQ ID NO:50, or SEQ ID NO:51 is, inherently, a nucleotide sequence of at least about 25-55 nucleotides that hybridizes with one or more disease-associated nucleic acids.

For claim 53, support for the recitation of “40 or more contiguous nucleotides” is found, *inter alia*, on page 5, lines 6-9 of the originally filed specification.

For claim 56, support for the recitation of “100 or more contiguous amino acids” is found, *inter alia*, on page 13, lines 20-23 of the originally filed specification.

Claim objections

Claims 52, 53, and 74 have been objected to for referring to sequences and SNPs contained in tables in the instant application (Office Action, page 2). The Examiner has cited MPEP §2173(s), and noted that it is possible to refer to the claimed sequences and SNPs using proper sequence identifiers and phraseology (Office Action, pages 2-3).

As a result of this Amendment, claim 74 has been cancelled without disclaimer or prejudice, solely to expedite prosecution of the instant application (see above). In addition, claim 52 has been amended to recite specific sequence identifiers, and claim 53 has been amended to recite specific sequence identifiers and nucleotide positions. The amendments to claims 52 and 53 are fully supported by the originally filed application and contain no new matter (see above). It is believed that the cancellation of claim 74 and the amendments to claims 52 and 53 obviate this objection. Accordingly, withdrawal of the objection is respectfully requested.

35 U.S.C. §112, second paragraph

Claims 34-74 have been rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention (Office Action, page 3). Specifically, the Examiner has stated that:

- Claims 34-41, and 42-51 are indefinite over the recitation “a complementary nucleic acid sequence of SEQ ID NO:1”;
- Claims 34-41 and 56-63 are indefinite over the recitation “under stringent conditions”
- Claim 52 is indefinite over the recitation “any of the nucleic acids of table 5”;
- Claim 53 is indefinite over the recitations “nucleic acid molecule of SEQ ID NO:1” and “contains at least one single nucleotide polymorphism”;
- Claim 54 and 55 are indefinite over the recitation “BAC RP11-0702C13 of SEQ ID NO:1”;
- Claims 56-63 and 64-73 are indefinite over the recitation “a complementary nucleic acid of SEQ ID NO:2”;
- Claims 72 and 73 are indefinite over the recitation “a host cell according to claim 68”; and
- Claim 74 is indefinite over the recitation “An isolated variant of SEQ ID NO:2” (Office Action, pages 3-6).

Applicants respectfully traverse this rejection. As indicated previously, claims 43-45, 51, 55, 65-67, 69, 71, and 73-74 have been cancelled without disclaimer or prejudice, solely to expedite prosecution of the instant application (see above). In addition, claims 34, 42, 52-54, 56, 64, and 72 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). In particular:

- Claims 34 and 42 have been amended to recite “a complement of SEQ ID NO:1” in accordance with the Examiner's suggestion;
- Claim 34 and 56 have been amended to delete the recitation “under stringent conditions”;
- Claim 52 has been amended to delete the recitation “any of the nucleic acids of table 5”;
- Claim 53 has been amended to delete the recitations “nucleic acid molecule of SEQ ID NO:1” and “contains at least one single nucleotide polymorphism”;
- Claims 54 and 55 have been amended to recite “An isolated nucleic acid fragment of

BAC RP11-0702C13”;

- Claims 56 and 64 have been amended to recite “a complement of SEQ ID NO:2” in accordance with the Examiner’s suggestion; and
- Claim 72 has been amended to depend from claim 70.

It is noted that claims 35-41 ultimately depend from claim 34; claims 46, 48, and 50 ultimately depend from claim 42; claims 57-63 ultimately depend from claim 56; and claims 68, 70, and 72 ultimately depend from claim 64. It is believed that the claim cancellations and amendments obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

35 U.S.C. §§102(b) and 102(e)

Shankar et al.

Claims 34-38, 41-51, 52-55, 56-60, and 63-74 have been rejected under 35 U.S.C. §102(b) as being anticipated by Shankar et al., 1994, *Biochem. J.* **300**:295-298 (Office Action, pages 6-8). The Examiner states that Shankar et al. report the sequence published as GenBank Accession No. U04799, as well as vectors and host cells comprising this sequence (Office Action, pages 7-8).

The Examiner further states that the Shankar et al. sequence represents i) an isolated nucleic acid molecule comprising at least 50 nucleotides which would hybridize under stringent conditions to SEQ ID NO:1 (Office Action, page 6); ii) a nucleic acid that would be expected to hybridize to SEQ ID NO:2 (Office Action, page 7); and iii) a nucleic acid comprising at least 15 consecutive nucleotides of SEQ ID NO:49 (Office Action, page 8).

In addition, it is stated that:

- Nucleotides 2050-2504 of SEQ ID NO:1 are identical to nucleotides 566-1019 of the

Shankar et al. sequence (244 contiguous nucleotides);

- Nucleotides 570-1024 of SEQ ID NO:2 are identical to nucleotides 566-1019 of the Shankar et al. sequence (244 contiguous nucleotides);
- Nucleotides 13-39 of SEQ ID NO:49 are identical to nucleotides 1373-1399 of the Shankar et al. sequence (27 contiguous nucleotides; Office Action, pages 7-8).

Applicants respectfully traverse this rejection. As indicated previously, claims 43-45, 47, 49, 51, 55, 65-67, 69, 71, and 73-74 have been cancelled without prejudice or disclaimer (see above). In addition, claims 34, 42, 52-54, 56, and 64 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, these claims read:

34. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:1;
- (b) a complement of SEQ ID NO:1;
- (c) a nucleotide sequence comprising 289 or more contiguous nucleotides of SEQ ID NO:1;
- (d) a complement of (c);
- (e) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:1; and
- (f) a complement of (e).

42. (Once Amended) Isolated DNA or RNA comprising 289 or more contiguous nucleotides of:

- (a) SEQ ID NO:1; or
- (b) a complement of SEQ ID NO:1.

52. (Once Amended) An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
- (b) a complement of (a);
- (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51; and
- (d) a complement of (c).

53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1 and includes at least one

single nucleotide polymorphism selected from the group consisting of:

- (a) an A at position 6684;
- (b) a G at position 6684;
- (c) a C at position 6991;
- (d) a T at position 6991;
- (e) a C at position 3176; and
- (f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides of SEQ ID NO:1.

56. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:2;
- (b) a nucleotide sequence encoding amino acid sequence SEQ ID NO:3;
- (c) a complement of SEQ ID NO:2;
- (d) a nucleotide sequence comprising 289 or more contiguous nucleotides of SEQ ID NO:2;
- (e) a complement of (d);
- (f) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:2;
- (g) a complement of (f); and
- (h) a nucleotide sequence which encodes 100 or more consecutive amino acids of SEQ ID NO:3.

64. (Once Amended) Isolated DNA or RNA comprising 289 or more contiguous nucleotides of:

- (a) SEQ ID NO:2; or
- (b) a complement of SEQ ID NO:2.

These amendments are fully supported by the originally filed application and introduce no new matter (see above). As before, it is noted that claims 35-41 ultimately depend from claim 34; claims 46, 48, and 50 ultimately depend from claim 42; claims 57-63 ultimately depend from claim 56; and claims 68, 70, and 72 ultimately depend from claim 64. It is believed that the claim cancellations and amendments obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

BACPAC RPCI-11 filters

Claims 34-37, 42-47, 52-55, 56-59, 64-69, and 74 have been rejected under §102(b) as being anticipated by the public use or sale of the BACPAC RPCI-11 filters (Office Action, page 8). The Examiner states that the filters include an isolated nucleic acid that would hybridize under stringent conditions to SEQ ID NO:1 (Office Action, page 8). The Examiner further states that the filters represent: i) nucleic acids that would comprise at least 50 consecutive nucleotides of SEQ ID NO:1; ii) nucleic acids that would comprise at least 50 consecutive nucleotides of SEQ ID NO:2; iii) nucleic acids comprising three SNPs in Table 5; and iv) nucleic acids that encode the amino acid sequence of SEQ ID NO:3 (Office Action, pages 8-9).

Applicants respectfully traverse this rejection. First, it is again noted that claims 43-45, 47, 49, 51, 55, 65-67, 69, 71, and 73-74 have been cancelled without prejudice or disclaimer (see above). Second, it is respectfully asserted that the BACPAC RPCI-11 filters do not anticipate or make obvious the subject matter of any of the claims of the instant application, including claims 34-37, 42, 46, 52-54, 56-59, 64, and 68. The BACPAC RPCI-11 filters do not represent isolated nucleic acids. Rather, the filters represent extremely large mixtures of unidentified nucleotide sequences.

To illustrate this, Applicants have attached hereto the publication describing the construction of the RPCI-11 library (Osoegawa et al., 2001, *Genome Res.* 11:483-496). The RPCI-11 library has been estimated to contain 543,797 total clones with an estimated insert size of 163-195 kb (Table 1; Osoegawa et al.). This means that the RPCI-11 library contains approximately 97 Mb of human DNA. Therefore, the RPCI-11 library, and filters derived therefrom, do not represent isolated nucleic acids such as SEQ ID NO:1, SEQ ID NO:2, or their

variants. Rather the BACPAC RPCI-11 filters represent a hodgepodge of undifferentiated nucleic acids. In no way can the filters be construed to teach the isolated, specific sequences that are Applicants' claimed invention.

Notably, it is the identification and isolation of the nucleic acids of SEQ ID NO:1, SEQ ID NO:2, and their variants that constitutes an important contribution of Applicants' invention. Applicants disclose in detail the extensive experimentation required to identify and isolate the claimed sequences. In particular, Applicants point to pages 40-63 of the specification as originally filed (Sections D-H). In addition, the instant application defines "isolated" nucleic acids as:

nucleic acids separated away from the nucleic acids of the genomic DNA or cellular RNA of their source of origin (*e.g.*, as it exists in cells or in a mixture of nucleic acids such as a library), and may have undergone further processing (page 10, lines 17-20 of the originally filed specification).

Therefore, because Applicants claim isolated, specific nucleic acids, whereas the BACPAC RPCI-11 filters contain large mixtures of unidentified nucleic acids, the sale or knowledge of the BAC filters do not anticipate or make obvious the claimed invention. Withdrawal of the rejection is respectfully requested.

GenBank Accession No. AA463832

Claims 52, 53, and 54 have been rejected under 35 U.S.C. §102(b) as being anticipated by the sequence published as GenBank Accession No. AA463832 (Office Action, page 9). The Examiner states that the AA463832 sequence represents a nucleic acid comprising at least 15 consecutive nucleotides of SEQ ID NO:46 that include a SNP shown in Table 5 (Office Action, page 9). The Examiner further states that nucleotides 11-36 of SEQ ID NO:46 are identical to the complement of nucleotides 51-76 of the AA463832 sequence (26 contiguous nucleotides).

The AA463832 sequence is also stated to comprise at least 15 consecutive nucleotides of BAC RP11-0702C13 of SEQ ID NO:1 (Office Action, page 9).

Applicants respectfully traverse this rejection. As indicated above, claims 52, 53, and 54 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, the claims read:

52. (Once Amended) An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
- (b) a complement of (a);
- (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51; and
- (d) a complement of (c).

53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1 and includes at least one single nucleotide polymorphism selected from the group consisting of:

- (a) an A at position 6684;
- (b) a G at position 6684;
- (c) a C at position 6991;
- (d) a T at position 6991;
- (e) a C at position 3176; and
- (f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides of SEQ ID NO:1.

It is believed that the amendments to claims 52, 53, and 54 obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

GenBank Accession No. AC000367

Claims 52, 53, and 54 have been rejected under 35 U.S.C. §102(b) as being anticipated by the sequence published as GenBank Accession No. AC000367 (Office Action, page 9). The Examiner states that the AC000367 sequence represents a nucleic acid comprising at least 15

consecutive nucleotides of SEQ ID NO:47 that include a SNP shown in Table 5 (Office Action, page 9). The Examiner further states that nucleotides 3-22 of SEQ ID NO:47 are identical to nucleotides 32851-32870 of the AC000367 sequence (20 contiguous nucleotides). The AC000367 sequence is also stated to comprise at least 15 consecutive nucleotides of BAC RP11-0702C13 of SEQ ID NO:1 (Office Action, page 10).

Applicants respectfully traverse this rejection. As indicated before, claims 52, 53, and 54 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, the claims read:

52. (Once Amended) An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
- (b) a complement of (a);
- (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51; and
- (d) a complement of (c).

53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1 and includes at least one single nucleotide polymorphism selected from the group consisting of:

- (a) an A at position 6684;
- (b) a G at position 6684;
- (c) a C at position 6991;
- (d) a T at position 6991;
- (e) a C at position 3176; and
- (f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides of SEQ ID NO:1.

It is believed that the amendments to claims 52, 53, and 54 obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

Tikoo et al.

Claims 52, 53, 54, and 74 have been rejected under 35 U.S.C. §102(e) as being anticipated by a sequence reported by Tikoo et al., U.S. Patent No. 6,319,716 (Office Action, page 10). The Examiner states that the Tikoo et al. sequence (SEQ ID NO:35) represents a nucleic acid comprising at least 15 consecutive nucleotides of SEQ ID NO:48 that include a SNP shown in Table 5 (Office Action, page 10). The Examiner further states that nucleotides 7-21 of SEQ ID NO:47 are identical to nucleotides 13657-13671 of the Tikoo et al. sequence (15 contiguous nucleotides). The Tikoo et al. sequence is also stated to comprise at least 15 consecutive nucleotides of BAC RP11-0702C13 of SEQ ID NO:1 (Office Action, page 10).

Applicants respectfully traverse this rejection. As previously indicated, claim 74 has been cancelled without prejudice or disclaimer, solely for the purpose of expediting the patent application process (see above). Also, claims 52, 53, and 54 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, the claims read:

52. (Once Amended) An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
 - (b) a complement of (a);
 - (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51;
- and
- (d) a complement of (c).

53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1 and includes at least one single nucleotide polymorphism selected from the group consisting of:

- (a) an A at position 6684;
- (b) a G at position 6684;
- (c) a C at position 6991;
- (d) a T at position 6991;

- (e) a C at position 3176; and
- (f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides of SEQ ID NO:1.

It is believed that the cancellation of claim 74 and the amendments to claims 52, 53, and 54 obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

WO 85/02610

Claims 52, 53, and 54 have been rejected under 35 U.S.C. §102(b) as being anticipated by a sequence published in WO 85/02610 (Office Action, page 10). The Examiner states that the WO 85/02610 sequence (found on page 43) represents a nucleic acid comprising at least 15 consecutive nucleotides of SEQ ID NO:50 that include a SNP shown in Table 5 (Office Action, page 10). The Examiner further states that nucleotides 14-28 of SEQ ID NO:50 are identical to nucleotides 248-262 of the WO 85/02610 sequence (15 contiguous nucleotides). The WO 85/02610 sequence is also stated to comprise at least 15 consecutive nucleotides of BAC RP11-0702C13 of SEQ ID NO:1 (Office Action, page 10).

Applicants respectfully traverse this rejection. As previously indicated, claims 52, 53, and 54 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, the claims read:

52. (Once Amended) An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
 - (b) a complement of (a);
 - (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51; and
 - (d) a complement of (c).

53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1 and includes at least one single nucleotide polymorphism selected from the group consisting of:

- (a) an A at position 6684;
- (b) a G at position 6684;
- (c) a C at position 6991;
- (d) a T at position 6991;
- (e) a C at position 3176; and
- (f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides of SEQ ID NO:1.

It is believed that the amendments to claims 52, 53, and 54 obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

35 U.S.C. §103(a)

Claims 39, 40, 61, and 62 have been rejected under 35 U.S.C. §103(a) as being unpatenable over Shankar et al. in view of Lasky et al., U.S. Patent No. 5,304,640 (Office Action, page 11). The Examiner states that Shankar et al. report a nucleic acid molecule that comprises 50 nucleotides which hybridize under stringent conditions to SEQ ID NO:1 (Office Action, page 11). According to the Examiner, the Shankar et al. sequence would hybridize under high stringency conditions to SEQ ID NO:1 and SEQ ID NO:2 (Office Action, pages 11-12).

In addition, the Examiner states that nucleotides 2050-2504 of SEQ ID NO:1 are identical to nucleotides 566-1019 of the Shankar et al. sequence (244 contiguous nucleotides); and nucleotides 570-1024 of SEQ ID NO:2 are identical to nucleotides 566-1019 of the Shankar et al. sequence (244 contiguous nucleotides; Office Action, pages 11-12). The Examiner notes that Shankar et al. fail to teach human host cells. The Examiner states that the Lasky et al. report typical eukaryotic host cells, such as CHO and 293 cells (Office Action, page 12). The

Examiner concludes that it would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to transform human host cells with vectors containing the nucleic acid reported by Shankar et al. (Office Action, pages 12-13).

Applicants respectfully traverse this rejection. As indicated previously, claims 34 and 56 have been amended to clarify and more fully describe Applicants' invention, as well as to expedite prosecution (see above). As presently amended, these claims read:

34. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:1;
- (b) a complement of SEQ ID NO:1;
- (c) a nucleotide sequence comprising 289 or more contiguous nucleotides of SEQ ID NO:1;
- (d) a complement of (c);
- (e) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:1; and
- (f) a complement of (e).

56. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:2;
- (b) a nucleotide sequence encoding amino acid sequence SEQ ID NO:3;
- (c) a complement of SEQ ID NO:2;
- (d) a nucleotide sequence comprising 289 or more contiguous nucleotides of SEQ ID NO:2;
- (e) a complement of (d);
- (f) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:2;
- (g) a complement of (f); and
- (h) a nucleotide sequence which encodes 100 or more consecutive amino acids of SEQ ID NO:3.

It is noted that claims 39 and 40 are ultimately dependent on claim 34, and claims 61 and 62 are ultimately dependent on claim 56. It is believed that the amendments to claims 34 and 56 obviate this ground of rejection. Withdrawal of the rejection is therefore respectfully requested.

Examiner's conclusion

The Examiner has concluded that claims directed to an isolated nucleic acid consisting of SEQ ID NO:1 or the complement of SEQ ID NO:1 would be allowable. The Examiner has further concluded that claims directed to an isolated nucleic acid consisting of SEQ ID NO:2 or the complement of SEQ ID NO:2 would be allowable (Office Action, page 13).

CONCLUSION

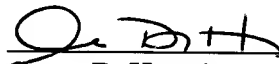
Applicants believe that the claims of the subject application are in condition for allowance. An action passing this case to issue is courteously urged. In the event that the Examiner is of the opinion that further discussion of the application would be helpful, the Examiner is hereby respectfully requested to telephone the Applicants' undersigned representative at (212) 415-8742 and is assured of full cooperation in an effort to advance the prosecution of the instant application and claims to allowance.

AUTHORIZATION

The Commissioner is hereby authorized to charge any additional fees which may be required for the timely consideration of this amendment under 37 C.F.R. §§ 1.16 and 1.17, or credit any overpayment to Deposit Account No. 13-4500, Order No. 2976-4037. A DUPLICATE COPY OF THIS SHEET IS ATTACHED.

Respectfully submitted,
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Dated: November 19, 2002

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APPENDIX**MARKED VERSION OF CLAIMS SHOWING AMENDMENTS MADE**

34. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- (a) SEQ ID NO:1;
- (b) a complement[ary nucleic acid sequence] of SEQ ID NO:1; [and]
- (c) a [nucleic acid] nucleotide sequence comprising [at least 50] 289 or more contiguous nucleotides [which hybridizes under stringent conditions to] of SEQ ID NO:1[.];
- (d) a complement of (c);
- (e) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:1; and
- (f) a complement of (e).

37. (Once Amended) An expression vector [containing] comprising the nucleic acid molecule of claim 34.

38. (Once Amended) A host cell [containing] comprising the vector of claim 37.

42. (Once Amended) Isolated DNA or RNA comprising [at least 50 consecutive] 289 or more contiguous nucleotides of:

- (a) SEQ ID NO:1[.]; or
- (b) a complement[ary nucleic acid sequence] of SEQ ID NO:1.

43. Cancelled.

44. Cancelled.

45. Cancelled.

46. (Once Amended) An expression vector [containing] comprising the DNA or RNA of claim 42.
47. Cancelled.
48. (Once Amended) A host cell [containing] comprising the vector of claim 46.
49. Cancelled.
51. Cancelled.
52. (Once Amended) [A] An isolated polynucleotide comprising [at least 15 consecutive nucleotides of any of the nucleic acids of Table 5, wherein the 15 consecutive nucleotides include a single nucleotide polymorphism (SNP) site selected from Table 5] a nucleotide sequence selected from the group consisting of:
- (a) SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:49;
 - (b) a complement of (a);
 - (c) a nucleotide sequence comprising at least 25 contiguous nucleotides of any one of SEQ ID NO:48, SEQ ID NO:50, and SEQ ID NO:51; and
 - (d) a complement of (c).
53. (Once Amended) An isolated nucleic acid molecule which comprises 40 or more contiguous nucleotides of SEQ ID NO:1[, wherein the nucleic acid molecule contains at least one single nucleotide polymorphism (SNP) of Table 5] and includes at least one single nucleotide polymorphism selected from the group consisting of:
- (a) an A at position 6684;
 - (b) a G at position 6684;
 - (c) a C at position 6991;
 - (d) a T at position 6991;

(e) a C at position 3176; and

(f) a T at position 3176.

54. (Once Amended) An isolated nucleic acid fragment of BAC RP11-0702C13 which comprises 289 or more contiguous nucleotides [comprising at least 15 consecutive nucleotide bases of BAC RP11-0702C13] of SEQ ID NO:1.

55. Cancelled.

56. (Once Amended) An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) SEQ ID NO:2;

(b) a [nucleic acid] nucleotide sequence encoding amino acid sequence SEQ ID NO:3;

(c) a complement[ary nucleic acid sequence] of SEQ ID NO:2; [and]

(d) a [nucleic acid] nucleotide sequence comprising 289 or more contiguous nucleotides of [at least 50 nucleotides which hybridizes under stringent conditions to] SEQ ID NO:2[.];

(e) a complement of (d);

(f) a nucleotide sequence comprising 500 or more contiguous nucleotides of SEQ ID NO:2;

(g) a complement of (f); and

(h) a nucleotide sequence which encodes 100 or more consecutive amino acids of SEQ ID NO:3.

59. (Once Amended) An expression vector [containing] comprising the nucleic acid molecule of claim 56.

60. (Once Amended) A host cell [containing] comprising the vector of claim 59.

64. (Once Amended) Isolated DNA or RNA comprising [at least 50 consecutive] 289 or more contiguous nucleotides of:
(a) SEQ ID NO:2[,]; or
(b) a complement[ary nucleic acid sequence] of SEQ ID NO:2.
65. Cancelled.
66. Cancelled.
67. Cancelled.
68. (Once Amended) An expression vector [containing] comprising the DNA or RNA of claim 64.
69. Cancelled.
70. (Once Amended) A host cell [containing] comprising the vector of claim 68.
71. Cancelled.
72. (Once Amended) The host cell according to claim [68] 70 selected from the group consisting of a eukaryotic cell, a human cell and a prokaryotic cell.
73. Cancelled.
74. Cancelled.